

#55, 60

RESULT 7

S38908

glutathione reductase (NADPH) (EC 1.6.4.2) - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 03-Nov-2000

C;Accession: S38908

R;Creissen, G.; Mullineaux, X.Y.Z.

submitted to the EMBL Data Library, November 1993

A;Reference number: S38908

A;Accession: S38908

A;Molecule type: mRNA

A;Residues: 1-557 <CRE>

A;Cross-references: EMBL:X76293; NID:g431954; PIDN:CAA53925.1; PID:g431955

C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology

C;Keywords: FAD; flavoprotein; NADP; oxidoreductase; redox-active disulfide

F;83-528/Domain: dihydrolipoamide dehydrogenase homology <DLD>

F;127-132/Disulfide bonds: redox-active #status predicted

Query Match 27.5%; Score 791.5; DB 2; Length 557;
Best Local Similarity 38.0%; Pred. No. 1.3e-49;
Matches 186; Conservative 82; Mismatches 196; Indels 25; Gaps 13;

Qy 54 NGPEDLPKSYDYDLIIIGGGSGGLAAAKEAAQYGKKVMV--LDFVTPTPLGTRWGLGGTC 111
|| | |: ||:| | ||||: |: :| | | | : | |:| |
Db 70 NG-ADAPRHYDFDLFTIGAGSGGVRASRFASNFGASVAVCELPFSTISSDST-GGVGGTC 127

Qy 112 VNVGCIPIPKLMHQAAALLGQALQDSRNYGWKVEETVKHWDWMIEAVQNHIGSLNWGYRVA 171
| ||:| ||: | : :| :| : : | | : | : | :
Db 128 VLRGCVPKLLVYASKYSHEFEESCGFGWNYDVEPRFDWSTLIANKNAELQRLTGIYKNI 187

Qy 172 LREKKVYENAYGQFIGPHRIKATNNKGKEKIYSAERFLIATGERPRYLGI PGDKEYCIS 231
|: | |: : | : |: ||: ||: | || || | ||
Db 188 LKNAGVTLEGRGKVDPHTVDVDG-----KLYSAKNILISVGGRPFIPDIPG-SEY AID 241

Qy 232 SDDLFLPYCPGKTLVVGASYVALECA GFLAGIGLDVTVMVR-SILLRGFDQDMANKIGE 290
|| || | | :| |:| | | |: :| | :| :| ||||: : : ||
Db 242 SDAALDLPTKPNKIAIVGGGYIALEFAGIFNGLKSEVHV FIRQKVLRGFDEEIRDFVGE 301

Qy 291 HMEEHGIKFIRQFVPIKVEQIEAGTPGRLRVVAQSTNSEEIIIEGEYNTVMLAIGRDACTR 350
| ||:| : | : | | : | :| : : | | | | :
Db 302 QMSLRGIEFHTEESP---QAIVKSADGSLSL----KTSRGTV EG-FSHIMFATGRRPNTK 353

Qy 351 KIGLETVGVKINEKTGKIPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGRLLAQRLY 410
: ||||| |: | | | : :| | |:| |:| |:| |:| |:| |:| : :
Db 354 NLGLETVGVKMT-KNGAIEVDEYSRTSVPSIWAVGDV-TDRINLTPVALMEGGALAKTIF 411

Qy 411 AGSTVKCDYENVPTTFTPTPLEYGACGLSEEKAVEKFGEENIEVYHSYFWPLEWTIPSRDN 470
| | | | | |: | | | |:| |:| |:| |:| |:| |:| :
Db 412 AHEPTKPDYRNVPAAVFSQPPIGQVGLMEEQAIKEFGD--VDVYTANFRPLKATISGLPD 469

Qy 471 NKCYAKIICNTKDNERVVG FHVLPNAGEVTQGFAAALKCGLTKKQLDSTIGIHPVCAEV 530
|: | :| :| :| :| | | | |:| | | | |:| | | |
Db 470 RVFMKLIVC--AKTSKVLGLHMC GDDAPEIVQGFAIAVKAGLTKADFDATVGIHPTS AEE 527

Qy 531 FTTL SVTKR 539
| | : |

Db 528 FVTMRTPTR 536